

SEQUENCE LISTING

<110> Piddington, Christopher S.
Bishop, Paul D.

<120> ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG
ZACRP2

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<151> 2000-04-19

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agggttaacca cc atg atc ccc tgg gtg ctc ctg gcc tgt gcc ctc ccc tgt 171
Met Ile Pro Trp Val Leu Leu Ala Cys Ala Leu Pro Cys
1 5 10

gct gct gac cca ctg ctt ggc gcc ttt gct cgc agg gac ttc cgg aaa 219
Ala Ala Asp Pro Leu Leu Gly Ala Phe Ala Arg Arg Asp Phe Arg Lys
15 20 25

ggc tcc cct caa ctg gtc tgc agc ctg cct ggc ccc cag ggc cca ccc 267
Gly Ser Pro Gln Leu Val Cys Ser Leu Pro Gly Pro Gln Gly Pro Pro
30 35 40 45

ggc ccc cca gga gcc cca ggg ccc tca gga atg atg gga cga atg ggc 315
Gly Pro Pro Gly Ala Pro Gly Pro Ser Gly Met Met Gly Arg Met Gly
50 55 60

ttt cct ggc aaa gac ggc caa gat gga cac gac ggc gac cgg ggg gac 363
Phe Pro Gly Lys Asp Gly Gln Asp Gly His Asp Gly Asp Arg Gly Asp
65 70 75

agc gga gag gaa ggt cca cct ggc cgg aca ggt aac cgg gga aag cca 411
Ser Gly Glu Gly Pro Pro Gly Arg Thr Gly Asn Arg Gly Lys Pro
80 85 90

gga cca aag ggc aaa gcc ggg gcc att ggg cgg gct ggc ccc cgt ggc 459
Gly Pro Lys Gly Lys Ala Gly Ala Ile Gly Arg Ala Gly Pro Arg Gly
95 100 105

ccc aag ggg gtc aac ggt acc ccc ggg aag cat ggc aca cca ggc aag	507
Pro Lys Gly Val Asn Gly Thr Pro Gly Lys His Gly Thr Pro Gly Lys	
110 115 120 125	
aag ggg ccc aag ggc aag aaa ggg gag cca ggc ctc cca ggc ccc tgc	555
Lys Gly Pro Lys Gly Lys Gly Glu Pro Gly Leu Pro Gly Pro Cys	
130 135 140	
agc tgt ggc agt ggc cat acc aag tca gct ttc tcg gtg gca gtg acc	603
Ser Cys Gly Ser Gly His Thr Lys Ser Ala Phe Ser Val Ala Val Thr	
145 150 155	
aag agc tac cca cgg gag cgg ctg ccc atc aag ttt gac aag att ctg	651
Lys Ser Tyr Pro Arg Glu Arg Leu Pro Ile Lys Phe Asp Lys Ile Leu	
160 165 170	
atg aac gag ggt ggc cac tac aat gct tcc agc ggc aag ttc gtc tgc	699
Met Asn Glu Gly Gly His Tyr Asn Ala Ser Ser Gly Lys Phe Val Cys	
175 180 185	
ggc gtg cct ggg atc tac tac ttc acc tac gac atc acg ctg gcc aac	747
Gly Val Pro Gly Ile Tyr Tyr Phe Thr Tyr Asp Ile Thr Leu Ala Asn	
190 195 200 205	
aag cac ctg gcc atc ggc ctg gtg cac aac ggc cag tac cgc atc cgg	795
Lys His Leu Ala Ile Gly Leu Val His Asn Gly Gln Tyr Arg Ile Arg	
210 215 220	
acc ttt gat gcc aac acc ggc aac cac gat gtg gcc tca ggc tcc acc	843
Thr Phe Asp Ala Asn Thr Gly Asn His Asp Val Ala Ser Gly Ser Thr	
225 230 235	
atc ctg gct ctc aag cag ggt gac gaa gtt tgg ctg cag atc ttc tac	891
Ile Leu Ala Leu Lys Gln Gly Asp Glu Val Trp Leu Gln Ile Phe Tyr	
240 245 250	
tca gag cag aac ggg ctc ttc tat gac cct tac tgg aca gac agc ctc	939
Ser Glu Gln Asn Gly Leu Phe Tyr Asp Pro Tyr Trp Thr Asp Ser Leu	
255 260 265	
ttt acg ggc ttc cta atc tat gcc gac cag gat gac ccc aac gag gta	987
Phe Thr Gly Phe Leu Ile Tyr Ala Asp Gln Asp Asp Pro Asn Glu Val	
270 275 280 285	
tagacatgcc acggcggtcc tccaggcagg gaacaagctt ctggacttgg gcttacagag	1047
caagacccca caactgtagg ctgggggtgg ggggtcagat gagcgttct agcctcaggc	1107
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20 25 30	
Gln Leu Val Cys Ser Leu Pro Gly Pro Gln Gly Pro Pro Gly Pro Pro	
35 40 45	
Gly Ala Pro Gly Pro Ser Gly Met Met Gly Arg Met Gly Phe Pro Gly	

50	55	60
Lys Asp Gly Gln Asp Gly His Asp Gly Asp Arg Gly Asp Ser Gly Glu		
65	70	75
Glu Gly Pro Pro Gly Arg Thr Gly Asn Arg Gly Lys Pro Gly Pro Lys		80
85	90	95
Gly Lys Ala Gly Ala Ile Gly Arg Ala Gly Pro Arg Gly Pro Lys Gly		
100	105	110
Val Asn Gly Thr Pro Gly Lys His Gly Thr Pro Gly Lys Lys Gly Pro		
115	120	125
Lys Gly Lys Lys Gly Glu Pro Gly Leu Pro Gly Pro Cys Ser Cys Gly		
130	135	140
Ser Gly His Thr Lys Ser Ala Phe Ser Val Ala Val Thr Lys Ser Tyr		
145	150	155
Pro Arg Glu Arg Leu Pro Ile Lys Phe Asp Lys Ile Leu Met Asn Glu		160
165	170	175
Gly Gly His Tyr Asn Ala Ser Ser Gly Lys Phe Val Cys Gly Val Pro		
180	185	190
Gly Ile Tyr Tyr Phe Thr Tyr Asp Ile Thr Leu Ala Asn Lys His Leu		
195	200	205
Ala Ile Gly Leu Val His Asn Gly Gln Tyr Arg Ile Arg Thr Phe Asp		
210	215	220
Ala Asn Thr Gly Asn His Asp Val Ala Ser Gly Ser Thr Ile Leu Ala		
225	230	235
Leu Lys Gln Gly Asp Glu Val Trp Leu Gln Ile Phe Tyr Ser Glu Gln		240
245	250	255
Asn Gly Leu Phe Tyr Asp Pro Tyr Trp Thr Asp Ser Leu Phe Thr Gly		
260	265	270
Phe Leu Ile Tyr Ala Asp Gln Asp Asp Pro Asn Glu Val		
275	280	285

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 <213> Homo sapiens

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Lys Gly Ala Cys Thr Gly Trp Met Ala Gly Ile Pro Gly His Pro Gly			
35	40	45	
His Asn Gly Ala Pro Gly Arg Asp Gly Arg Asp Gly Thr Pro Gly Glu			
50	55	60	
Lys Gly Glu Lys Gly Asp Pro Gly Leu Ile Gly Pro Lys Gly Asp Ile			
65	70	75	80
Gly Glu Thr Gly Val Pro Gly Ala Glu Gly Pro Arg Gly Phe Pro Gly			
85	90	95	
Ile Gln Gly Arg Lys Gly Glu Pro Gly Glu Gly Ala Tyr Val Tyr Arg			
100	105	110	
Ser Ala Phe Ser Val Gly Leu Glu Thr Tyr Val Thr Ile Pro Asn Met			
115	120	125	
Pro Ile Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn His Tyr Asp			
130	135	140	
Gly Ser Thr Gly Lys Phe His Cys Asn Ile Pro Gly Leu Tyr Tyr Phe			
145	150	155	160
Ala Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe			
165	170	175	
Lys Lys Asp Lys Ala Met Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Asn			
180	185	190	

Asn	Val	Asp	Gln	Ala	Ser	Gly	Ser	Val	Leu	Leu	His	Leu	Glu	Val	Gly
195							200					205			
Asp	Gln	Val	Trp	Leu	Gln	Val	Tyr	Gly	Glu	Gly	Glu	Arg	Asn	Gly	Leu
210							215				220				
Tyr	Ala	Asp	Asn	Asp	Asn	Asp	Ser	Thr	Phe	Thr	Gly	Phe	Leu	Leu	Tyr
225							230				235			240	
His	Asp	Thr	Asn												

<210> 4
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<400> 4															
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								20		25			30		
Tyr	Gly	Ile	Pro	Gly	Met	Pro	Gly	Leu	Pro	Gly	Ala	Pro	Gly	Lys	Asp
								35		40			45		
Gly	Tyr	Asp	Gly	Leu	Pro	Gly	Pro	Lys	Gly	Glu	Pro	Gly	Ile	Pro	Ala
								50		55			60		
Ile	Pro	Gly	Ile	Arg	Gly	Pro	Lys	Gly	Gln	Lys	Gly	Glu	Pro	Gly	Leu
								65		70			75		80
Pro	Gly	His	Pro	Gly	Lys	Asn	Gly	Pro	Met	Gly	Pro	Pro	Gly	Met	Pro
								85		90			95		
Gly	Val	Pro	Gly	Pro	Met	Gly	Ile	Pro	Gly	Glu	Pro	Gly	Glu	Gly	
								100		105			110		
Arg	Tyr	Lys	Gln	Lys	Phe	Gln	Ser	Val	Phe	Thr	Val	Thr	Arg	Gln	Thr
								115		120			125		
His	Gln	Pro	Pro	Ala	Pro	Asn	Ser	Leu	Ile	Arg	Phe	Asn	Ala	Val	Leu
								130		135			140		
Thr	Asn	Pro	Gln	Gly	Asp	Tyr	Asp	Thr	Ser	Thr	Gly	Lys	Phe	Thr	Cys
								145		150			155		160
Lys	Val	Pro	Gly	Leu	Tyr	Tyr	Phe	Val	Tyr	His	Ala	Ser	His	Thr	Ala
								165		170			175		
Asn	Leu	Cys	Val	Leu	Leu	Tyr	Arg	Ser	Gly	Val	Lys	Val	Val	Thr	Phe
								180		185			190		
Cys	Gly	His	Thr	Ser	Lys	Thr	Asn	Gln	Val	Asn	Ser	Gly	Gly	Val	Leu
								195		200			205		
Leu	Arg	Leu	Gln	Val	Gly	Glu	Val	Trp	Leu	Ala	Val	Asn	Asp	Tyr	
								210		215			220		
Tyr	Asp	Met	Val	Gly	Ile	Gln	Gly	Ser	Asp	Ser	Val	Phe	Ser	Gly	Phe
								225		230			235		240
Leu	Leu	Phe	Pro	Asp											
				245											

<210> 5
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<220>
 <223> Aromatic motif

<221> VARIANT
 <222> (2)...(6)
 <223> Each Xaa is independently any amino acid residue.

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<221> VARIANT
<222> (7)...(7)
<223> Xaa is asparagine or aspartic acid.

<221> VARIANT
<222> (8)...(11)
<223> Each Xaa is independently any amino acid residue.

<221> VARIANT
<222> (12)...(12)
<223> Xaa is phenylalanine, tyrosine, tryptophan or
leucine.

<221> VARIANT
<222> (13)...(18)
<223> Each Xaa is independently any amino acid residue.

<221> VARIANT
<222> (20)...(24)
<223> Each Xaa is independently any amino acid residue.

<221> VARIANT
<222> (26)...(26)
<223> Xaa is any amino acid residue.

<221> VARIANT
<222> (28)...(28)
<223> Xaa is any amino acid residue.

<221> VARIANT
<222> (30)...(30)
<223> Xaa is any amino acid residue.

<221> VARIANT
<222> (31)...(31)
<223> Xaa is phenylalanine or tyrosine.

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Xaa Xaa Phe Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Phe Xaa Xaa
  20          25          30

<210> 6
<211> 17
<212> DNA
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<223> Degenerate nucleotide primer

<221> variation
<222> (1)...(17)
<223> n = A, T, G or C

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ggngansarg tntggyt
<210> 7

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<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Degenerate nucleotide primer

<221> variation
<222> (1)...(18)
<223> n = A, T, G or C

<400> 7
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<210> 8
<211> 17
<212> DNA
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<220>
<223> Degenerate nucleotide primer

<221> variation
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<223> n = A, T, G or C

<400> 8
ttydsnngnt tyytnht 17

<210> 9
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<221> variation
<222> (1)...(18)
<223> n = A, T, G or C

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<210> 10
<211> 855
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<221> variation
<222> (1)...(855)
<223> n = A, T, G or C

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 garggnccnc cnggnmgnac ngnnaaymgn gnaarcngc gnccnaargg naargcnggn 300
 gcnathggnm gngcnggncc nmgngnccn aarggngtna ayggnaacncc ngnnaarcay 360
 ggnacnccng gnaaraargg nccnaargg aaraarggg arccngnyt nccnggnccn 420
 tgywsntgyg gnwsnggnca yacnaarwsn gcnttywsng tngcngtnac naarwsntay 480
 ccnmgngarm gnytnccnat haarttyg aarathytta tgaaygargg ngncaaytay 540
 aaygcnwsn sngnaartt ygtntgygg gtnccnggn ahtaytayt yacntayg 600
 athacnytng cnaayaarca yytngcnath gnytngtnc ayaayggnc aytaymgnath 660
 mgnacnccng aycnaayac ngncaaycay gaygtngcnw snggnwsnac nathytngn 720
 ytnaarcarg gngaygargt ntggycnac ahttytayw sngarcaraa yggnytnty 780
 taygayccnt aytggacnng ywsnytnty acnggnccn tnathtaygc ngaycargay 840
 gayccnaayg argtn 855

<210> 11
 <211> 536
 <212> DNA
 <213> *Mus musculus*

<220>
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<221> variation
 <222> (1)...(536)
 <223> n = A, T, G or C

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tcc agt ggc aag ttc gtc tgc agc gtg ccg ggg atc tna tta cnt tta	96
Ser Ser Gly Lys Phe Val Cys Ser Val Pro Gly Ile Xaa Leu Xaa Leu	
20 25 30	

cct atg aca tta cgc ntg gcc aac aaa cac ctn gnc atc ggc ctg gtg	144
Pro Met Thr Leu Arg Xaa Ala Asn Lys His Leu Xaa Ile Gly Leu Val	
35 40 45	

cac aat ggt cag tac cgc att cgg act ttt gat gcc aac acg ggc aac	192
His Asn Gly Gln Tyr Arg Ile Arg Thr Phe Asp Ala Asn Thr Gly Asn	
50 55 60	

cac gac gtg gcc tcg ggc tcc acc atc cta gct ctc aag gag ggt gat	240
His Asp Val Ala Ser Gly Ser Thr Ile Leu Ala Leu Lys Glu Gly Asp	
65 70 75 80	

gaa gtc tgg ctg cag atc ttc tac tca gag cag aat ggc ctc ttc tac	288
Glu Val Trp Leu Gln Ile Phe Tyr Ser Glu Gln Asn Gly Leu Phe Tyr	
85 90 95	

gac cct tac tgg acc gac agc ctg ttc acc ggc ttc ctc atc tac gct	336
Asp Pro Tyr Trp Thr Asp Ser Leu Phe Thr Gly Phe Leu Ile Tyr Ala	
100 105 110	

gac caa gga gac ccc aac gag gta tagacaagcc ggggttgagc cttgaggtag	390
Asp Gln Gly Asp Pro Asn Glu Val	
115 120	

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<221> VARIANT
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<223> Xaa is any amino acid

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Pro Met Thr Leu Arg Xaa Ala Asn Lys His Leu Xaa Ile Gly Leu Val
 35          40          45
His Asn Gly Gln Tyr Arg Ile Arg Thr Phe Asp Ala Asn Thr Gly Asn
 50          55          60
His Asp Val Ala Ser Gly Ser Thr Ile Leu Ala Leu Lys Glu Gly Asp
 65          70          75          80
Glu Val Trp Leu Gln Ile Phe Tyr Ser Glu Gln Asn Gly Leu Phe Tyr
 85          90          95
Asp Pro Tyr Trp Thr Asp Ser Leu Phe Thr Gly Phe Leu Ile Tyr Ala
100          105          110
Asp Gln Gly Asp Pro Asn Glu Val
115          120

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<223> Oligonucleotide ZC20810

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<210> 14
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